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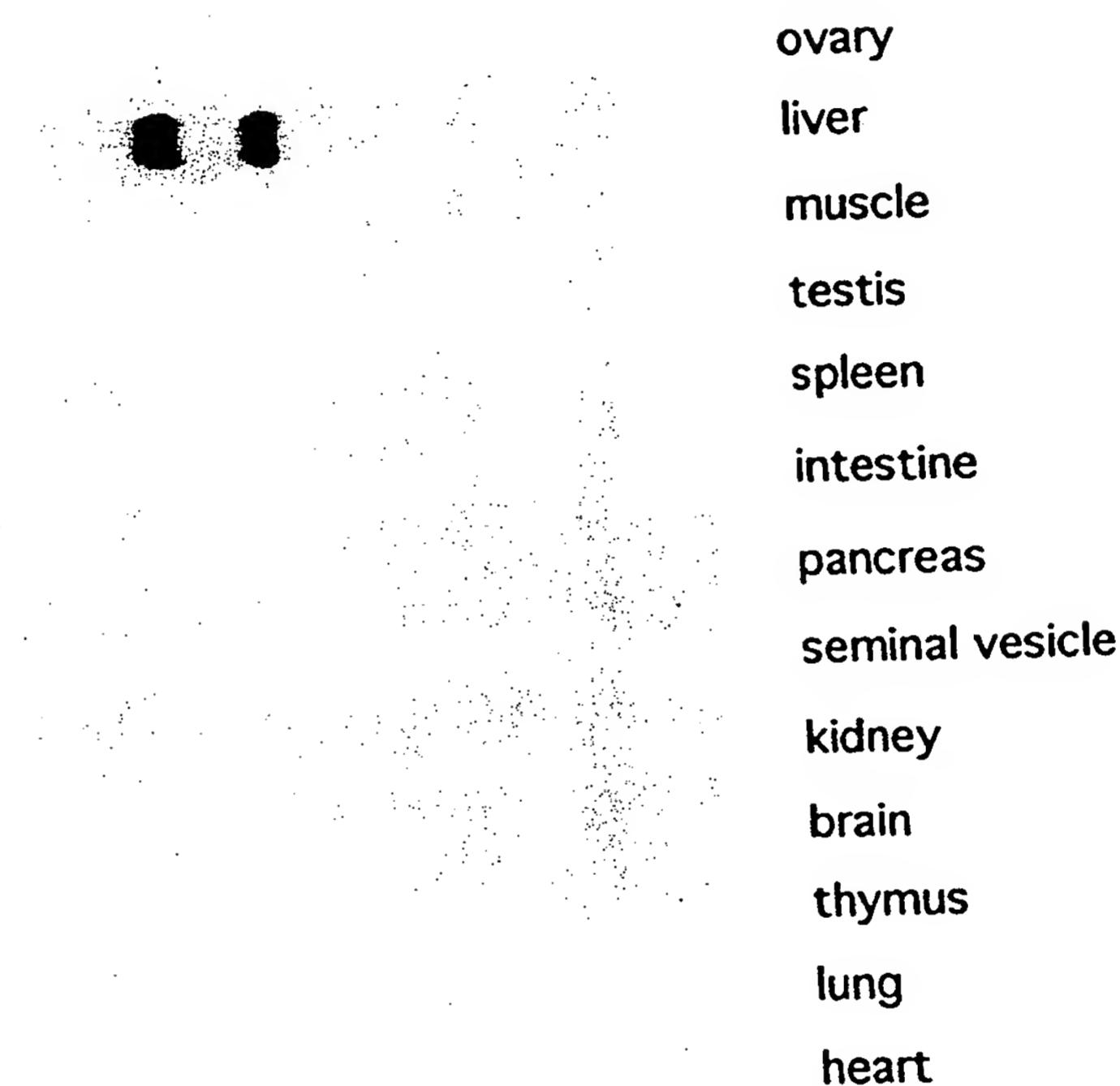


FIG. 1

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1 CGGGCCAGGAGGAGGACCCCCACCTGTGAGCCTGCCACCCCTTATGTTCGCAGGCCAGAC 60
R A R R R T P T C E P A T P L C C R R D
61 CATTACGTAGACTTCAGGAACCTGGATGGCGGGACTGGATACTGCAGCCCAGGGTAC 120
H Y V D F Q E L G W R D W I L Q P E G Y
121 CAGCTGAATTACTGCAGTGGCCAGTGCCCTCCCCACCTGGCTGGCAGCCCAGGCATGGCT 180
Q L N Y C S G Q C P P H L A G S P G I A
181 GCCTCTTCCATTCTGCCGTCTCAGCCTCTCAAAGCCAACAATCCTGGCCTGCCAGT 240
A S F H S A V F S L L K A N N P W P A S
241 ACCTCCTGTTGTGTCCCTACTGCCCGAAGGCCCTCTCTCTACCTGGATCATAAT 300
T S C C V P T A R R P L S L L Y L D H N
301 GGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCTGTGGCTGCAGCTAG 360
G N V V K T D V P D M V V E A C G C S *

FIG. 2

<u>Family member</u>	<u>% identity with GDF-12</u>
GDF-1	43
GDF-3	36
GDF-5	36
GDF-6	39
GDF-7	42
GDF-9	30
BMP-3	37
BMP-2	43
BMP-4	42
Vgr-1	41
OP-1	40
BMP-5	38
OP-2	39
MIS	30
Inhibin- α	27
Inhibin- β A	47
Inhibin- β B	50
Nodal	38
GDNF	21
TGF- β 1	36
TGF- β 2	36
TGF- β 3	41

FIG. 4

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1	GAGCTGTGAGGGTCAAGCACAGCTATCCATCAGATGATCTACTTCAGCCTTCCTGAGTC	60
61	CCAGACAAATAGAAGACAGGTGGCTGTACCCCTGGCCAAGGGTAGGTGTGGCAGTGGTGTC	120
121	TGCTGTCACTGTGCCCTCATGGCCCCCAGCAATCAGACTAACAGACGGAGCAACTGCC	180
181	ATCCGAGGCTCCTGAACCAGGGCATTCAACCAGGAGCATGCCGCTCCCTGATGTCCAGCT	240
	M R L P D V Q L	
241	CTGGCTGGTGCTGCTGTGGCACTGGTGCAGGCACAGGGACAGGGCTGTGTGTCCTC	300
	W L V L L W A L V R A Q G T G S V C P S	
301	CTGTGGGGCTCAAACCTGGCACCCAAAGCAGAACGAGCTCTGGTGTGGAGCTAGCCAA	360
	C G G S K L A P Q A E R A L V L E L A K	
361	GCAGCAAATCCTGGATGGTGCACCTGACCAAGTGTCCCAGAATAACTCATCCTCCACC	420
	Q Q I L D G L H L T S R P R I T H P P P	
421	CCAGGCAGCGCTGACCAAGGCCCTCCGGAGACTACAGCCAGGGAGTGTGGCTCCAGGGAA	480
	Q A A L T R A L R R L Q P G S V A P G N	
481	TGGGGAGGAGGTCACTCAGCTTGCTACTGTACAGACTCCACTTCAGCCTACAGCTCCCT	540
	G E E V I S F A T V T D S T S A Y S S L	
541	GCTCACTTTCACCTGTCCACTCCTCGGTCCCACCACCTGTACCATGCCGCTGTGGCT	600
	L T F H L S T P R S H H L Y H A R L W L	
601	GCACGTGCTCCCCACCCTCCTGGCACTCTTGCTTGAGGATCTCCGATGGGACCAAG	660
	H V L P T L P G T L C L R I F R W G P R	
661	GAGGAGGGCCAAGGGTCCCGCACTCTCTGGCTGAGCACCACATACCAACCTGGCTG	720
	R R R Q G S R T L L A E H H I T N L G W	
721	GCATACCTTAACCTGCCCTCTAGTGGTTGAGGGTGAGAAGTCTGGTGTCCCTGAAACT	780
	H T L T L P S S G L R G E K S G V L K L	
781	GCAACTAGACTGCAGACCCCTAGAAGGAAACAGCACAGTTACTGGACAACCGAGGGCT	840
	Q L D C R P L E G N S T V T G Q P R R L	
841	CTTGGACACAGCAGGACACCAGCAGGCCCTCTAGAGCTTAAGATCCGAGCCAATGAGCC	900
	L D T A G H Q Q P F L E L K I R A N E P	
901	TGGAGCAGGCCGGCCAGGAGGAGGACCCCCACCTGTGAGCCTGGCACCCCTATGTTG	960
	G A G R A R R R T P T C E P A T P L C C	
961	CAGGCAGGACCAATTACGTAGACTTCCAGGAACCTGGATGGCGGGACTGGATACTGCAGCC	1020
	R R D H Y V D F Q E L G W R D W I L Q P	
1021	CGAGGGTACCAAGCTGAATTACTGCAGTGGCAGTGCCCTCCCCACCTGGCTGGCAGCCC	1080
	E G Y Q L N Y C S G Q C P P H L A G S P	
1081	AGGCATTGCTGCCCTTTCCATTCTGCCGTCTCAGCCTCCTCAAAGCCAACAATCCTTG	1140
	G I A A S F H S A V F S L L K A N N P W	
1141	GCCTGCCAGTACCTCCTGTTGTCCTACTGCCGAAGGCCCTCTCTCCTACCT	1200
	P A S T S C C V P T A R R P L S L L Y L	
1201	GGATCATAATGGCAATGTGGTCAAGACGGATGTGCCAGATATGGTGGTGGAGGCCGTGG	1260
	D H N G N V V K T D V P D M V V E A C G	
1261	CTGCAGCTAGCAAGAGGACCTGGGGCTTGGAGTGAAGAGACCAAGATGAAGTTCCCAG	1320
	C S *	
1321	GCACAGGGCATCTGTGACTGGAGGCATCAGATTCTGATCCACACCCAAACCAACACC	1380
1381	ACCTGGCAATATGACTCACTTGACCCCTATGGGACCCAAATGGGACTTTCTGTCTGAG	1440
1441	ACTCTGGCTTATTCCAGGTTGGCTGATGTGTGGAGATGGTAAAGCGTTCTTCTAAA	1500
1501	GGGGTCTACCCAGAAAGCATGATTCCTGCCCTAAGTCTGTGAGAAGATGTCAAGGGACT	1560
1561	AGGGAGGGAGGGAGGGAAAGGCAGAGAAAAATTACTTAGCCTCTCCAAGATGAGAAAGTC	1620
1621	CTCAAGTGAGGGAGGAAGCAGATAGATGGTCCAGCAGGCTTGAAGCAGGGTAAGCA	1680
1681	GGCTGGCCAGGGTAAGGGCTGTTGAGGTACCTTAAGGAAGGTCAAGAGGGAGATGGC	1740
1741	AAGGCCTGAGGGAGGATGCTTAGGGACCCCCAGAAAACAGGAGTCAGGAAATGAGGCA	1800
1801	CTAACGCTAACAGATTCCCTGGTTTTCCCAGGGACAGGACCCACTGGAGACAAGCAT	1860
1861	TTATACTTTCTTCTTTTATTTTGAGATCGAGTCCTCGCTCTGTCACCAGGCT	1920
1921	GGAGTGCAGTGACACGATCTGGCTCACTGCAACCTCCGTCTGGTTCAAGTGATT	1980
1981	TTCTGCCCTAGCCCTCCGAGCAGCTGGATTACAGGCGCCACTAATTGTTGATTCTTA	2040
2041	GTAGAAACGAGGTTCAACATGTTGCCAGGATGGCTCAATCTCTGACCTCTTGATCC	2100
2101	ACCCGACTTGGCTCCCGAAGTGATGAGATTAGGCAGTGAGCCACCGCGCTGGCTTAT	2160
2161	ACTTTCTTAATAAAAGGAGAAAGAAAATCAACAAATGTGAGTCATAAAGAAGGTTAGG	2220
2221	GTGATGGTCCAGACCAACAGTTCTCAAGTGTACTCTGAGGCTCTGGAGGTCCCTT	2280
2281	TCAGGGGTGTCCACAAAGCTAAAGCTATTTCATAATAACTAACATGTTATTGCCTT	2340
2341	TTGAATTCTCATTATCTTAAAATTGTATTGAGTTCCAGAGGCCGTGTGACATGTG	2400
2401	ATTACATCATCTTCTGAC 2419	